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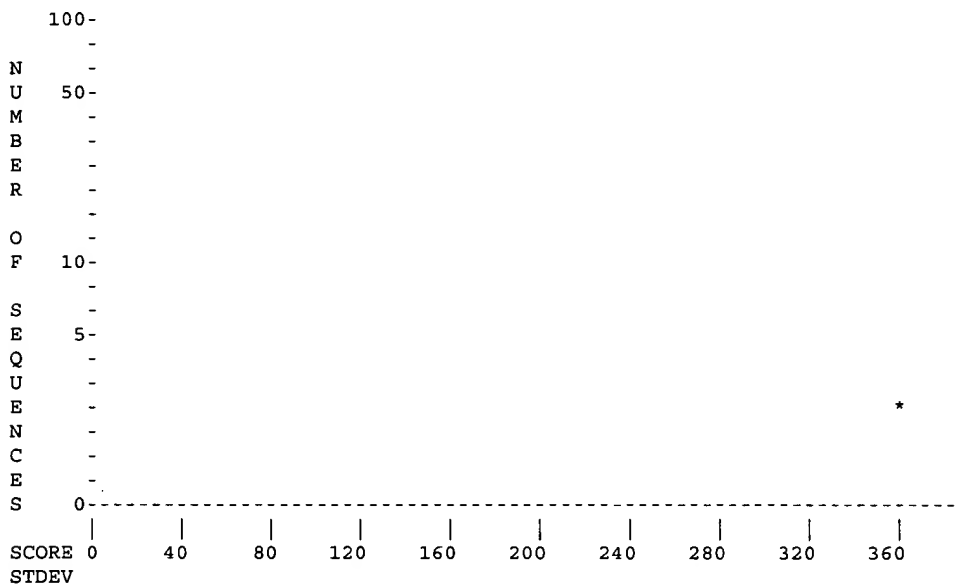
FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file seq2-seq4.res made by mruhl on Wed 29 Jan 103 17:52:07-PST.

Query sequence being compared:US-09-531-266-2 (1-360)

Number of sequences searched: 2  
Number of scores above cutoff: 2

Results of the initial comparison of US-09-531-266-2 (1-360) with:  
File : US09531266.pep



#### PARAMETERS

Similarity matrix	PAM-150	K-tuple	2
Threshold level of sim.	16%		
Mismatch penalty	1	Joining penalty	20
Gap penalty	5.00	Window size	360
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

#### SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	360	361	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	720
Number of sequences searched:	2
Number of scores above cutoff:	2

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-531-266-4	Sequence 4, Application US	360	360	360	0.00	0

1. US-09-531-266-2 (1-360)  
US-09-531-266-4 Sequence 4, Application US/09531266

Initial Score = 360 Optimized Score = 360 Significance = 0.00  
Residue Identity = 100% Matches = 360 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

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X      10      20      30      40      50      60      70
MSHIDDLAQLGTSTWLDDLSRERITSGNLSQVIEEKS VVGVTNPAIFAAAMSKGDSYDAQIAELKAAGASV
|||||
MSHIDDLAQLGTSTWLDDLSRERITSGNLSQVIEEKS VVGVTNPAIFAAAMSKGDSYDAQIAELKAAGASV
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
DQAVYAMSIDDVRNACDLFTGIFESSNGYDGRVSI EVDPRISADRDATLAQAKELWAKVDRPNVMIKIPATP
|||||
DQAVYAMSIDDVRNACDLFTGIFESSNGYDGRVSI EVDPRISADRDATLAQAKELWAKVDRPNVMIKIPATP
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
GSLPAITDALAEGISVNVTLIFSVARYREVIAAFIEGIKQAAANGHDVSKIHSVASFFVSRVDVEIDKRLEA
|||||
GSLPAITDALAEGISVNVTLIFSVARYREVIAAFIEGIKQAAANGHDVSKIHSVASFFVSRVDVEIDKRLEA
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
IGSDEALALRGKAGVANARAYAVYKELFDAAE LPEGANTQRPLWASTGVKNPAYAATLYVSELAGPNTVNT
|||||
IGSDEALALRGKAGVANARAYAVYKELFDAAE LPEGANTQRPLWASTGVKNPAYAATLYVSELAGPNTVNT
     220     230     240     250     260     270     280

    290     300     310     320     330     340     350     X
MPEGTIDAVLEQGNLHGDTLSNSAAEADAVFSQLEALGVLDLADV FQVLETEGVDKFVASWSELLESMEARLK
|||||
MPEGTIDAVLEQGNLHGDTLSNSAAEADAVFSQLEALGVLDLADV FQVLETEGVDKFVASWSELLESMEARLK
    290     300     310     320     330     340     350     360

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